

01/11

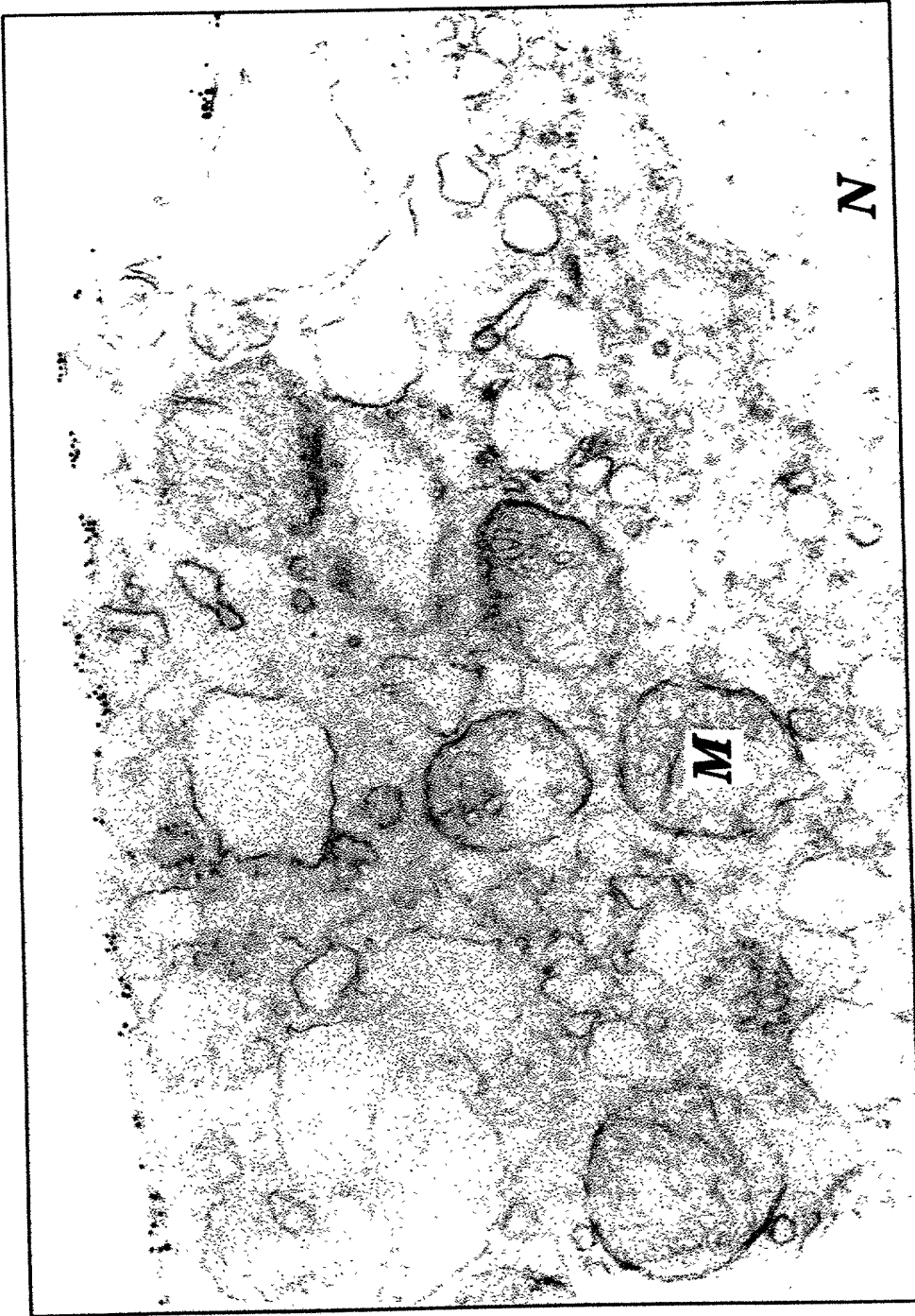


FIG. 1

099665 1001
T0402T" 59962660

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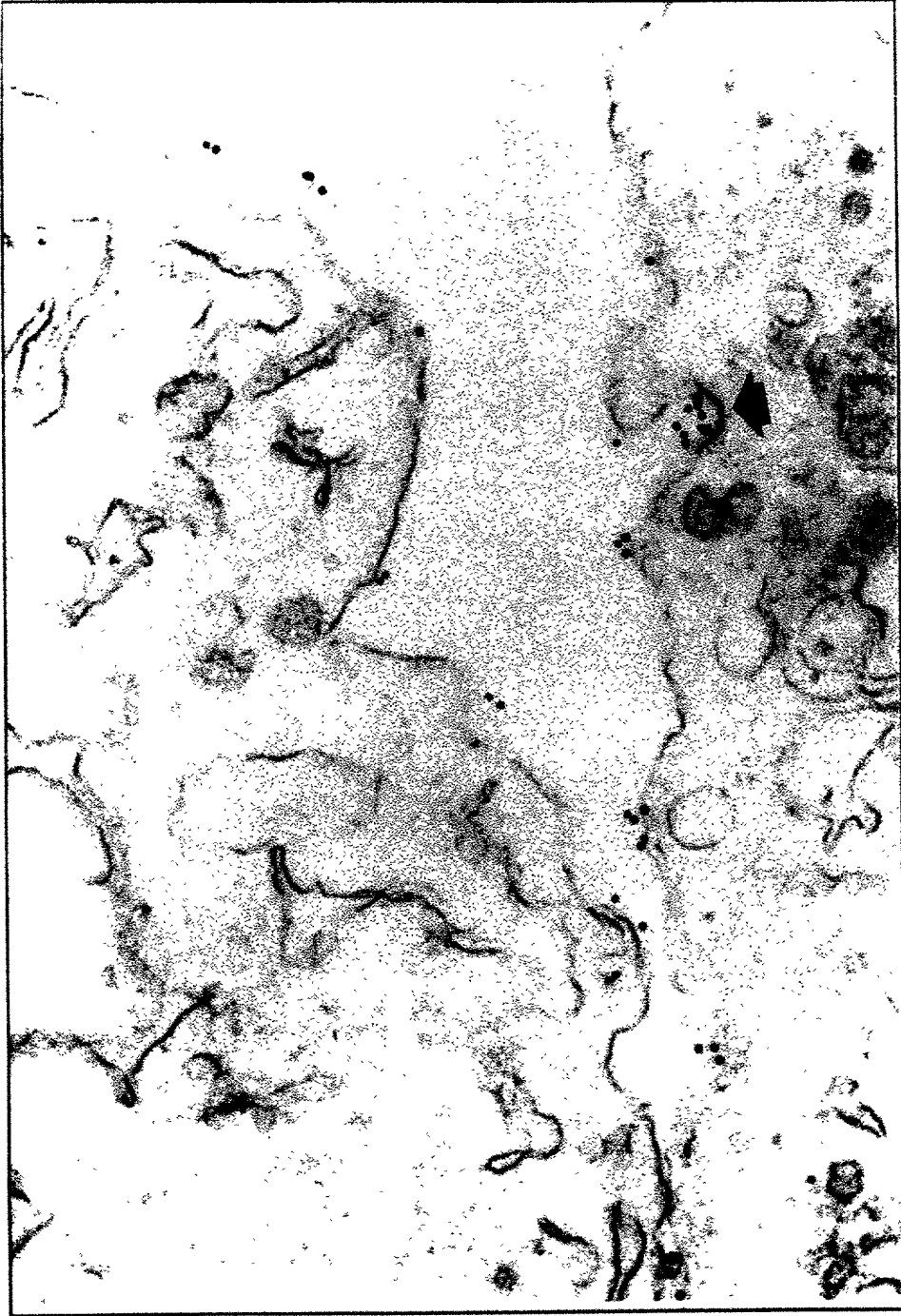


FIG. 2

09929665 "120701

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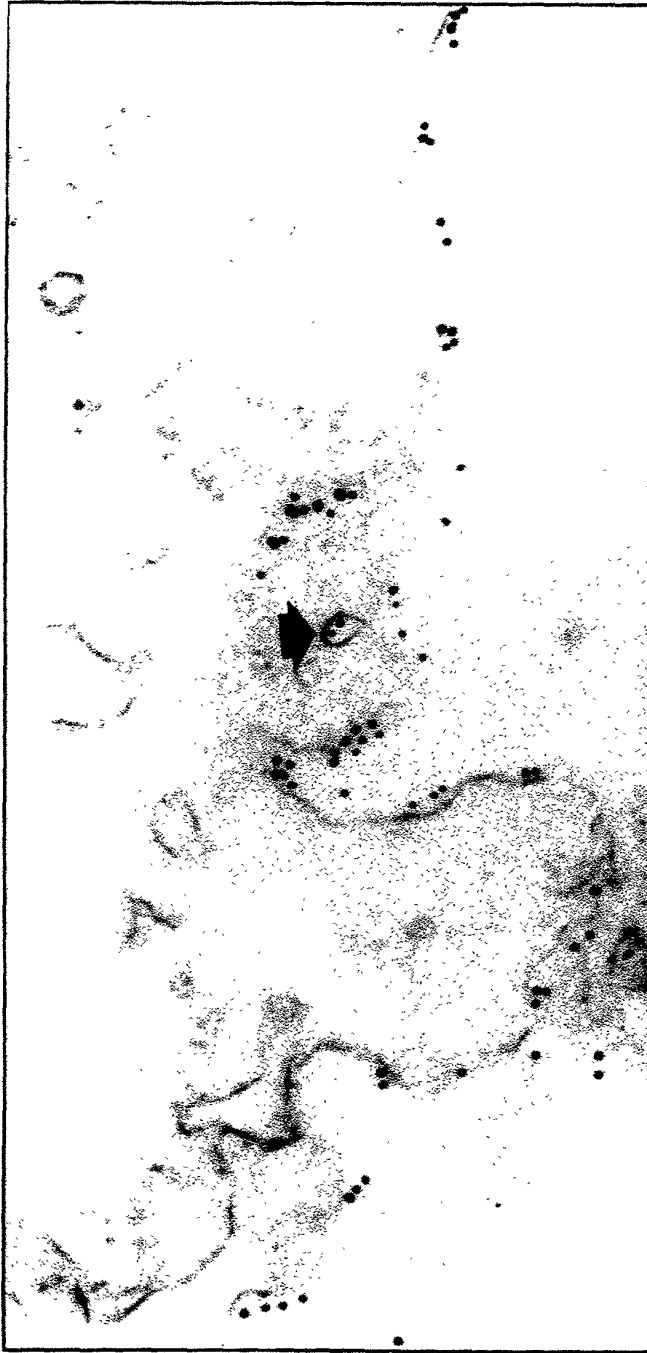


FIG. 3

FOOT " 59362660

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FIG. 4

0929665 12001

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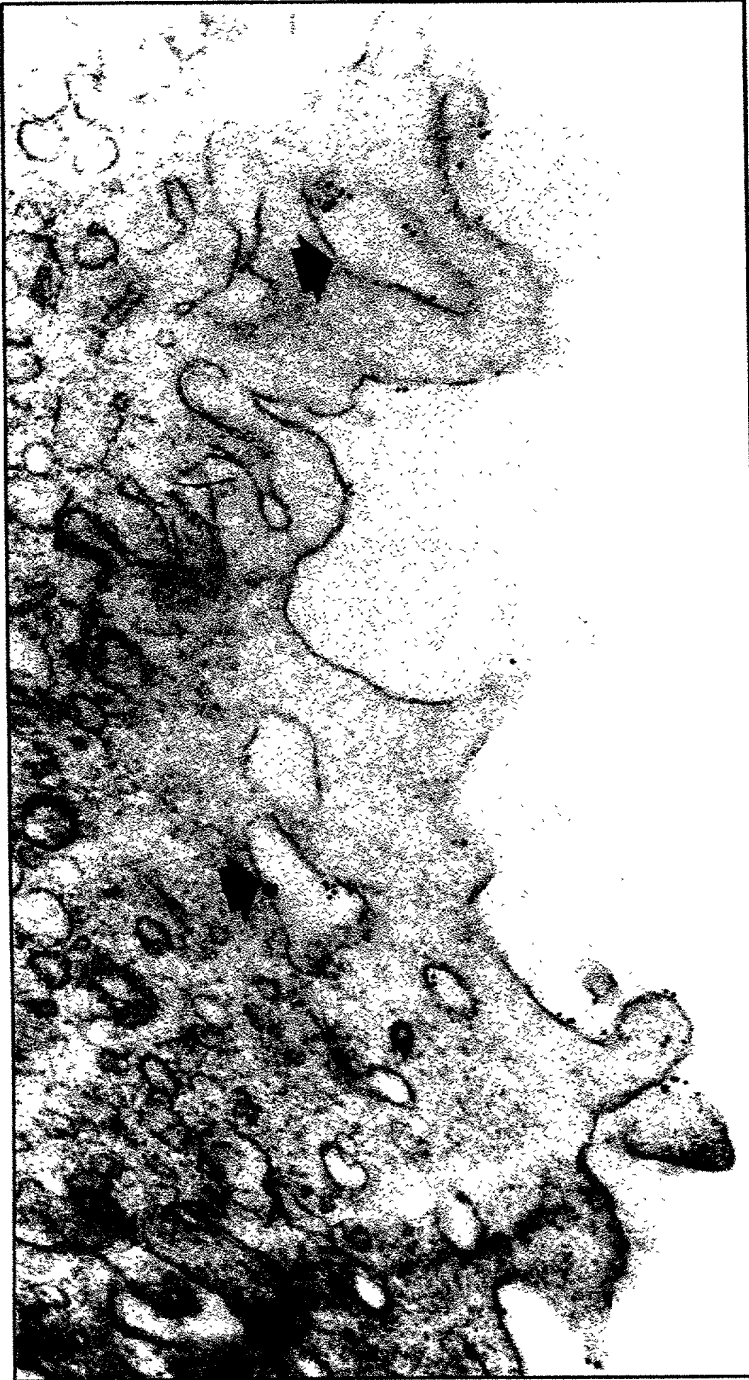


FIG. 5

09929665 - 120701

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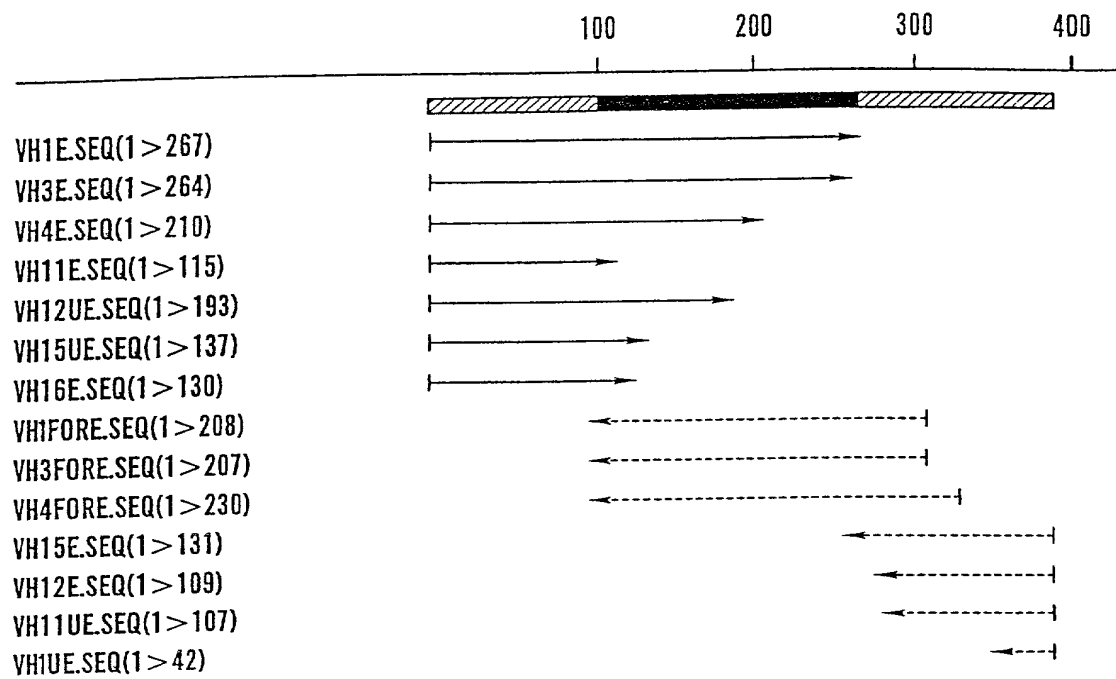


FIG. 6

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/929,665

07/11

ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

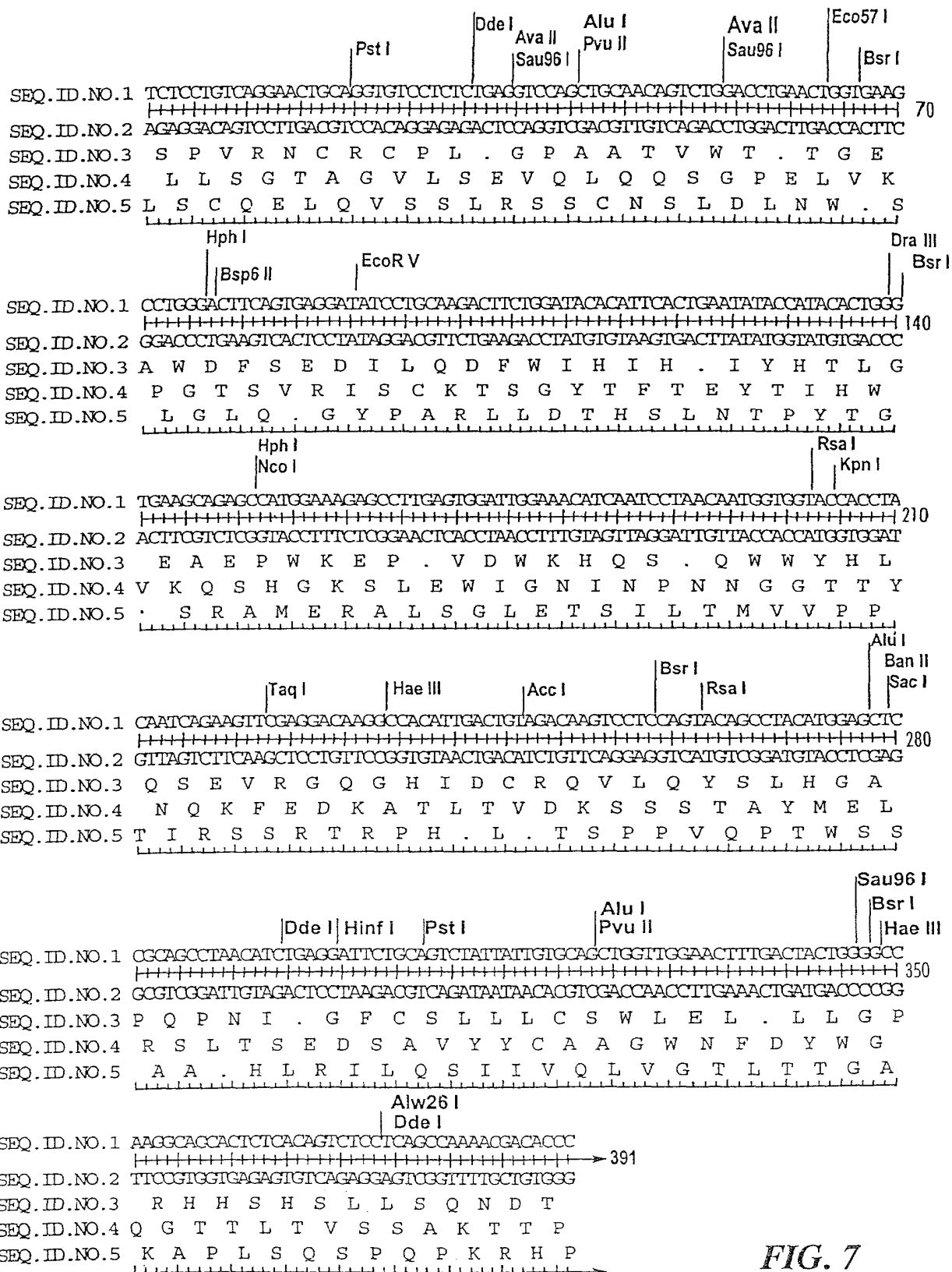


FIG. 7

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LIPMAN-PEARSON PROTEIN ALIGNMENT

KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115)	SEQ2(1>125)	SIMILARITY	GAP	GAP	CONSENSUS
J591VH.PRO	MUVHIIA.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>115)	(1>125)	75.6	2	10	125

EVQLQQSGPELVKPGTSVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGIT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFIDYMNWVKQSPGKSLEWIGDINPNNGGTS
YNQKFEDKATLTIVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGGIT
YNQKF.:KATLTIVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWGGIT
YNQKFKGKATLTIVDKSSSTAYMQLSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGIT

LTVSS
:TVSS
VTVSS

FIG. 8

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/929,665

09/11

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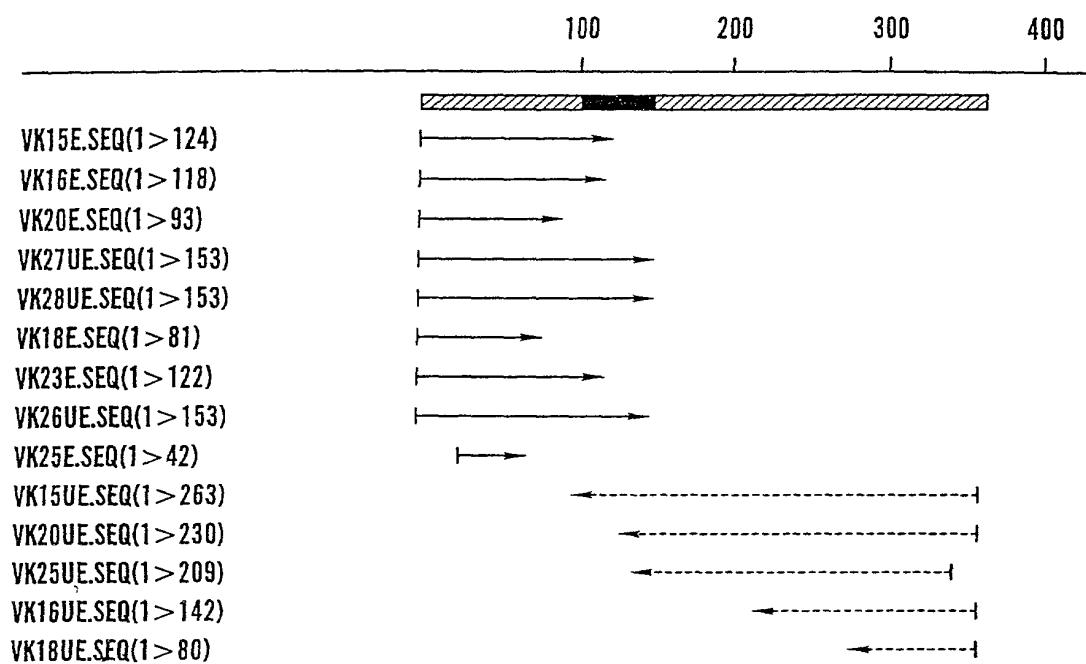


FIG. 9

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/929.665

10/11

ENZYMES: ALL 74 ENZYMES (NO FILTER):
 SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

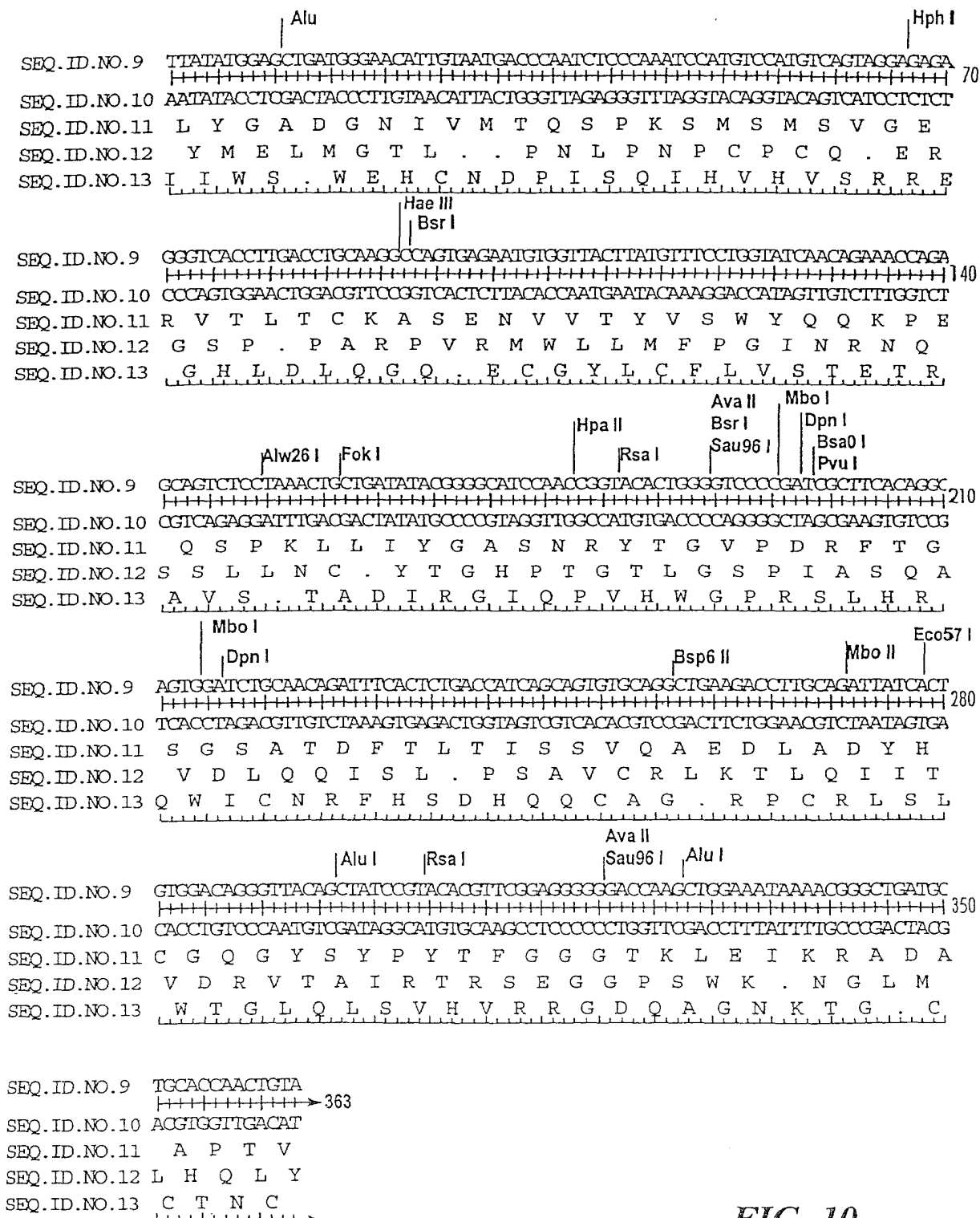


FIG. 10

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LIPMAN-PEARSON PROTEIN ALIGNMENT

KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107)	SEQ2(1>111)	SIMILARITY	GAP	GAP	CONSENSUS
J591VK.PRO	MUVKV.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>107)	(1>109)	60.4	2	2	109

↓10 ↓20 ↓30 ↓40 ↓50
NIVMTQSPKSMMSVGERVILTCKAS-ENVVTVVSWYQQKPEQSPKLLIYGASNRYTGVP
:I MIQSP.S:S S:G:RVT:TC:AS ::: .Y::WYQQKP. SPKLLIY AS. .:GVP
DIQMTQSPSSLSASLGDRVTITCRASQDDISNYLNWYQQKPEGGSPKLLIYYASRLHSGVP
↑10 ↑20 ↑30 ↑40 ↑50 ↑60
↓60 ↓70 ↓80 ↓90 ↓100
DRFTGSGSATDFTLTISVQAEDLADYHCGQGY-SY-PYTFGGGKLEIK
.RF:GSGS:TD::LTIS:::ED:A.Y C QG : P TFGGGKLEIK
SRFSGSGSGTDYSLTISNLEQEDIATYFQQGNLPPRTFSGGKLEIK
↑70 ↑80 ↑90 ↑100

FIG. 11